

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 16:39:35 / Search time 34 Seconds

(without alignments)
289.440 Million cell updates/sec

Title: US-10-004-381-25

Perfect score: 258
Sequence: 1 MDEKTTGWRGHHVEGLAGE.....LEHHQGRPPMSSGCKLG 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	47	14	US-10-004-381-25
2	243	94.2	47	14	US-10-004-381-26
3	241	93.4	61	14	US-10-004-381-24
4	234	90.7	75	14	US-10-004-381-23
5	227	88.0	89	14	US-10-004-381-22
6	214	82.9	101	14	US-10-004-381-21
7	211	81.8	101	14	US-10-004-381-19
8	208	80.6	38	14	US-10-004-381-35
9	208	80.6	426	14	US-10-004-381-41
10	208	80.6	479	14	US-10-004-381-38
11	199	77.1	39	14	US-10-004-381-27
12	152	58.9	29	14	US-10-004-381-29
13	133	51.6	89	14	US-10-004-381-28
14	94	36.4	44	14	US-10-004-381-34
15	70	27.1	102	14	US-10-004-381-11

16	68	26.4	101	14	US-10-004-381-12	Sequence 12, Appl
17	66.5	25.8	739	15	US-10-156-761-13097	Sequence 13097, A
18	61	23.6	1181	15	US-10-156-761-12448	Sequence 12448, A
19	59.5	23.1	84	12	US-09-864-408A-6610	Sequence 6610, Ap
20	59.5	23.1	342	9	US-09-912-020-260	Sequence 260, App
21	59	22.9	139	12	US-10-094-749-2955	Sequence 2955, Ap
22	59	22.9	140	10	US-09-902-180-6	Sequence 6, Appl1
23	59	22.9	147	9	US-09-864-761-39307	Sequence 39307, A
24	59	22.9	1974	12	US-10-369-493-6395	Sequence 6395, Ap
25	58	22.5	2222	12	US-10-369-493-3923	Sequence 3923, Ap
26	57.5	22.3	1065	10	US-09-771-161A-239	Sequence 239, App
27	57	22.1	330	12	US-10-241-742-116	Sequence 116, App
28	57	22.1	330	15	US-10-146-772-116	Sequence 116, App
29	57	22.1	330	15	US-10-146-772-116	Sequence 116, App
30	57	22.1	474	10	US-09-738-626-6856	Sequence 6856, Ap
31	56.5	21.9	215	9	US-09-815-242-13710	Sequence 13710, A
32	56.5	21.9	986	12	US-10-114-153-50	Sequence 50, Appl
33	56	21.7	339	15	US-10-156-761-8695	Sequence 8695, Ap
34	56	21.7	374	11	US-09-975-719-29	Sequence 29, Appl
35	55.5	21.5	374	15	US-10-156-761-11951	Sequence 11951, A
36	55.5	21.5	1388	12	US-10-173-999-32	Sequence 32, Appl
37	55.5	21.5	1388	15	US-10-146-473-82	Sequence 82, Appl
38	55	21.3	243	12	US-10-369-493-12808	Sequence 12808, A
39	55	21.3	450	15	US-10-156-761-13613	Sequence 13613, A
40	55	21.3	605	12	US-10-094-749-2077	Sequence 2077, Ap
41	54.5	21.1	472	15	US-10-156-761-9474	Sequence 9474, Ap
42	54.5	21.1	5215	10	US-09-861-289-2	Sequence 2, Appl1
43	54.5	21.1	5215	10	US-09-860-846-2	Sequence 2, Appl1
44	54.5	21.1	5215	11	US-09-988-384B-2	Sequence 2, Appl1
45	54.5	21.1	5215	11	US-09-836-821-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-10-004-381-25
; Sequence 25, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-25
Query Match 100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.7e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0;
QY 1 MDEKTTGWRGHHVEGLAGELEQLRRLRLEHHQGRPPMSSGCKLG 47
DB 1 MDEKTTGWRGHHVEGLAGELEQLRRLRLEHHQGRPPMSSGCKLG 47
RESULT 2
US-10-004-381-26
; Sequence 26, Application US/10004381
; Publication No. US20020155578A1

GENERAL INFORMATION:
APPLICANT: SZOSTAK, JACK W.
APPLICANT: WILSON, DAVID S.
APPLICANT: KEEFE, ANTHONY D.
TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
FILE REFERENCE: 00786/388002
CURRENT FILING DATE: 2001-10-31
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO: 26
LENGTH: 47
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: selected peptide
US-10-004-381-26

Query Match 94.2%; Score 243; DB 14; Length 47;
Best Local Similarity 95.7%; Pred. No. 3.3e-24;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLHHHPQGGREPMMSSGCKLG 47
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLHHHPQGGREPMMSSGCKLG 47

RESULT 3
US-10-004-381-24
Sequence 24, Application US/10004381
Publication No. US20020155578A1
GENERAL INFORMATION:
APPLICANT: SZOSTAK, JACK W.
APPLICANT: WILSON, DAVID S.
APPLICANT: KEEFE, ANTHONY D.
TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
FILE REFERENCE: 00786/388002
CURRENT FILING DATE: 2001-10-31
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO: 24
LENGTH: 61
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: selected peptide
US-10-004-381-24

Query Match 93.4%; Score 241; DB 14; Length 61;
Best Local Similarity 77.0%; Pred. No. 7.9e-24;
Matches 47; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLHHHPQGGREPMMSSGCKLG 46
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLHHHPQGGREPMMSSGCKLG 60

QY 47 G 47
DB 61 G 61

RESULT 4
US-10-004-381-23
Sequence 23, Application US/10004381
Publication No. US20020155578A1
GENERAL INFORMATION:

APPLICANT: SZOSTAK, JACK W.
APPLICANT: WILSON, DAVID S.
APPLICANT: KEEFE, ANTHONY D.
TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
FILE REFERENCE: 00786/388002
CURRENT FILING DATE: 2001-10-31
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO: 23
LENGTH: 75
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: selected peptide
US-10-004-381-23

Query Match 90.7%; Score 234; DB 14; Length 75;
Best Local Similarity 62.7%; Pred. No. 8e-23; 0; Indels 28; Gaps 1;
Matches 47; Conservative 0; Mismatches 0;

QY 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLHHHPQGGREPMMSSGCKLG 38
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLHHHPQGGREPMMSSGCKLG 60

QY 39 -----MMSSGCKLG 47
DB 61 LLDPEVMMSSGCKLG 75

RESULT 5
US-10-004-381-22
Sequence 22, Application US/10004381
Publication No. US20020155578A1
GENERAL INFORMATION:
APPLICANT: SZOSTAK, JACK W.
APPLICANT: WILSON, DAVID S.
APPLICANT: KEEFE, ANTHONY D.
TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
FILE REFERENCE: 00786/388002
CURRENT FILING DATE: 2001-10-31
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO: 22
LENGTH: 89
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: selected peptide
US-10-004-381-22

Query Match 88.0%; Score 227; DB 14; Length 89;
Best Local Similarity 52.8%; Pred. No. 7.7e-22;
Matches 47; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLHHHPQGGREPMMSSGCKLG 38
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLHHHPQGGREPMMSSGCKLG 60

QY 39 -----MMSSGCKLG 47
DB 61 LLDPEVMMSSGCKLG 89

RESULT 6
US-10-004-381-21

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; Sequence 21, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-21

Query Match      82.9%; Score 214; DB 14; Length 101;
Best Local Similarity 44.6%; Pred. No. 4.3e-20;
Matches 45; Conservative 2; Mismatches 0; Indels 54; Gaps 1;

QY 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLEHHHPQGRPEPM----- 40
   |||||
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLEHHHPQGRPEPM----- 60
   |||||

QY 41 -----GGGCKLG 47
   |||||
DB 61 LIDPVEKLLTDMFKPKRNVSKCKMTFTYLEMTDWSGCKLG 101
   |||||

RESULT 7
US-10-004-381-19
; Sequence 19, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-19

Query Match      81.8%; Score 211; DB 14; Length 101;
Best Local Similarity 95.0%; Pred. No. 1.1e-19;
Matches 38; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLEHHHPQGRPEPM 40
   |||||
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLEHHHPQGRPEPLV 40
   |||||

RESULT 8
US-10-004-381-35
; Sequence 35, Application US/10004381
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; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-35

Query Match      80.6%; Score 208; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.8e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLEHHHPQGRPE 38
   |||||
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLEHHHPQGRPE 38
   |||||

RESULT 9
US-10-004-381-41
; Sequence 41, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed protein
US-10-004-381-41

Query Match      80.6%; Score 208; DB 14; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.2e-18;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGMRGHHVVEGLAGLEQLRLRLEHHHPQGRPE 38
   |||||
DB 378 MDEKTTGMRGHHVVEGLAGLEQLRLRLEHHHPQGRPE 415
   |||||

RESULT 10
US-10-004-381-38
; Sequence 38, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
```

;; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
;; FILE OF INVENTION: THEREOF
;; FILE REFERENCE: 00786/388002
;; CURRENT APPLICATION NUMBER: US/10/004,381
;; CURRENT FILING DATE: 2001-10-31
;; PRIOR APPLICATION NUMBER: US 60/244,541
;; PRIOR FILING DATE: 2000-10-31
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 38
;; LENGTH: 479
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Designed protein
US-10-004-381-38
Query Match 80.6%; Score 208; DB 14; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.4e-18;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGMRGSHVVEGLAGLEQLRLRLEHHPOGQREP 38
DB 378 MDEKTTGMRGSHVVEGLAGLEQLRLRLEHHPOGQREP 415
RESULT 11
US-10-004-381-27
; Sequence 27, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-27
Query Match 77.1%; Score 199; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GHVVEGLAGLEQLRLRLEHHPOGQREPMMGGCKLG 47
DB 3 GHVVEGLAGLEQLRLRLEHHPOGQREPMMGGCKLG 39
RESULT 12
US-10-004-381-29
; Sequence 29, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31

;; PRIOR APPLICATION NUMBER: US 60/244,541
;; PRIOR FILING DATE: 2000-10-31
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 29
;; LENGTH: 29
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: selected peptide
US-10-004-381-29
Query Match 58.9%; Score 152; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ELEGRLRLRLEHHPOGQREPMMGGCKLG 47
DB 2 ELEGRLRLRLEHHPOGQREPMMGGCKLG 29
RESULT 13
US-10-004-381-28
; Sequence 28, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-28
Query Match 51.6%; Score 133; DB 14; Length 89;
Best Local Similarity 35.6%; Pred. No. 1.2e-09;
Matches 31; Conservative 2; Mismatches 0; Indels 54; Gaps 1;

QY 15 EGLAGLEQLRLRLEHHPOGQREPMMGGCKLG 47
DB 3 EGLAGLEQLRLRLEHHPOGQREPMMGGCKLG 62
QY 41 -----SGGCKLG 47
DB 63 KFKNVSKDCKMTFYLEMYDWSGGCKLG 89
RESULT 14
US-10-004-381-34
; Sequence 34, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541

; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed peptide
US-10-004-381-34

Query Match 36.4%; Score 94; DB 14; Length 44;
Best Local Similarity 58.3%; Pred. No. 6.1e-05;
Matches 21; Conservative 3; Mismatches 4; Indels 8; Gaps 2;

QY 18 AGELEQLRAR-----LEHHPOGQREPPMMSGCKLG 47
DB 8 AGPVDQADARLVQGGALQHHPOGDR--MMSGCKLG 41

RESULT 15

US-10-004-381-11
; Sequence 11, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEPE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-11

Query Match 27.1%; Score 70; DB 14; Length 102;
Best Local Similarity 42.9%; Pred. No. 0.2;
Matches 18; Conservative 4; Mismatches 6; Indels 14; Gaps 3;

QY 1 MDEKTTGW--RGSHVVEGLAGELEQLRARLEHHPOGQREPPM 40
DB 1 MDEK-TMHERVHILADG-----LECHPOGQRRPLV 30

Search completed: February 6, 2004, 16:42:54
Job time : 36 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:14:57 ; Search time 21 Seconds
(without alignments)
215.235 Million cell updates/sec

Title: US-10-004-381-25

Perfect score: 47
Sequence: 1 MDEKTTGWRGCHVEGLAGE.....LEHHPOGQGRPPWMSGCKLG 47

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match length	ID	Description
No matches found					

Search completed: February 6, 2004, 17:15:32
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:14:57 ; Search time 11 Seconds
(without alignments)
200.932 Million cell updates/sec

Title: US-10-004-381-25

Perfect score: 47

Sequence: 1 MDEKTTGWRGSHVEGLAGE.....LEHHPOGQREPMMSGCKLG 47

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found					

Search completed: February 6, 2004, 17:16:43
Job time : 11 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:14:57 ; Search time 35 Seconds
(without alignments)
346.528 Million cell updates/sec

Title: US-10-004-381-25
Perfect score: 47
Sequence: 1 MDKTTGMRGCHVEGLAGE.....LEHHPOGQRPWMSGCKLG 47

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: February 6, 2004, 17:16:20
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:15:37 / Search time 21 Seconds
(without alignments)
94.696 Million cell updates/sec

Title: US-10-004-381-25
Perfect score: 47
Sequence: 1 MDEKTTGWRGCHVEGLAGE.....LEHHPOGGRFPMMGGCKLG 47

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Dackfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

No matches found

Search completed: February 6, 2004, 17:20:15
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:16:27 ; Search time 34 Seconds
(without alignments)
289.440 Million cell updates/sec

Title: US-10-004-381-25

Perfect score: 47
Sequence: 1 MDEKTTGMRGSHVEGLAGE.....LEHHPOGQREPMSGCKLG 47

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 801455 seqs, 209382283 residues

Word size : 10

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	47	US-10-004-381-25	Sequence 25, Appl
2	38	80.9	38	US-10-004-381-35	Sequence 35, Appl
3	38	80.9	61	US-10-004-381-24	Sequence 24, Appl
4	38	80.9	75	US-10-004-381-23	Sequence 23, Appl
5	38	80.9	89	US-10-004-381-22	Sequence 22, Appl
6	38	80.9	101	US-10-004-381-19	Sequence 19, Appl
7	38	80.9	101	US-10-004-381-21	Sequence 21, Appl
8	38	80.9	426	US-10-004-381-41	Sequence 41, Appl
9	38	80.9	479	US-10-004-381-38	Sequence 38, Appl
10	37	78.7	39	US-10-004-381-27	Sequence 27, Appl
11	31	66.0	47	US-10-004-381-26	Sequence 26, Appl
12	28	59.6	29	US-10-004-381-25	Sequence 29, Appl
13	24	51.1	89	US-10-004-381-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-10-004-381-25
; Sequence 25, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 25
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: selected peptide
US-10-004-381-25

Query Match 100.0%; Score 47; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.7e-41;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGMRGSHVEGLAGEQLRLRLEHHPOGQREPMSGCKLG 47
DB 1 MDEKTTGMRGSHVEGLAGEQLRLRLEHHPOGQREPMSGCKLG 47

RESULT 2
US-10-004-381-35
; Sequence 35, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 35
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: selected peptide
US-10-004-381-35

Query Match 80.9%; Score 38; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.7e-32;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGMRGSHVEGLAGEQLRLRLEHHPOGQREP 38
DB 1 MDEKTTGMRGSHVEGLAGEQLRLRLEHHPOGQREP 38

RESULT 3
US-10-004-381-24

```
; Sequence 24, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
; US-10-004-381-24
```

```
Query Match      80.9%; Score 38; DB 14; Length 61;
Best Local Similarity 100.0%; Pred. No. 8.6e-32;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDEKTTGMRGHHVVEGLAGLEQLRRLRLEHHPOGOREP 38
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRRLRLEHHPOGOREP 38
```

```
RESULT 4
; Sequence 23, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
; US-10-004-381-23
```

```
Query Match      80.9%; Score 38; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDEKTTGMRGHHVVEGLAGLEQLRRLRLEHHPOGOREP 38
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRRLRLEHHPOGOREP 38
```

```
RESULT 5
; Sequence 22, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
```

```
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
; US-10-004-381-22
```

```
Query Match      80.9%; Score 38; DB 14; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDEKTTGMRGHHVVEGLAGLEQLRRLRLEHHPOGOREP 38
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRRLRLEHHPOGOREP 38
```

```
RESULT 6
; Sequence 19, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
; US-10-004-381-19
```

```
Query Match      80.9%; Score 38; DB 14; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDEKTTGMRGHHVVEGLAGLEQLRRLRLEHHPOGOREP 38
DB 1 MDEKTTGMRGHHVVEGLAGLEQLRRLRLEHHPOGOREP 38
```

```
RESULT 7
; Sequence 21, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
```


; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 101
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-21

Query Match 80.9%; Score 38; DB 14; Length 101;
Best Local Similarity 100.0%; Pred. No. 1,3e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGWRGHHVVEGLAGELEQLRLRLHHHPQGQREP 38
DB 1 MDEKTTGWRGHHVVEGLAGELEQLRLRLHHHPQGQREP 38

RESULT 8
US-10-004-381-41
; Sequence 41, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 426
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed protein
US-10-004-381-41

Query Match 80.9%; Score 38; DB 14; Length 426;
Best Local Similarity 100.0%; Pred. No. 4,7e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGWRGHHVVEGLAGELEQLRLRLHHHPQGQREP 38
DB 378 MDEKTTGWRGHHVVEGLAGELEQLRLRLHHHPQGQREP 415

RESULT 9
US-10-004-381-38
; Sequence 38, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 38
; LENGTH: 479
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed protein
US-10-004-381-38

Query Match 80.9%; Score 38; DB 14; Length 479;
Best Local Similarity 100.0%; Pred. No. 5,2e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGWRGHHVVEGLAGELEQLRLRLHHHPQGQREP 38
DB 378 MDEKTTGWRGHHVVEGLAGELEQLRLRLHHHPQGQREP 415

RESULT 10
US-10-004-381-27
; Sequence 27, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 39
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: selected peptide
US-10-004-381-27

Query Match 78.7%; Score 37; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 6,2e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GHVEGLAGELEQLRLRLHHHPQGRPEPMMSGCKLG 47
DB 3 GHVEGLAGELEQLRLRLHHHPQGRPEPMMSGCKLG 39

RESULT 11
US-10-004-381-26
; Sequence 26, Application US/10004381
; Publication No. US20020155578A1
; GENERAL INFORMATION:
; APPLICANT: SZOSTAK, JACK W.
; APPLICANT: WILSON, DAVID S.
; APPLICANT: KEEFE, ANTHONY D.
; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
; FILE REFERENCE: 00786/388002
; CURRENT APPLICATION NUMBER: US/10/004,381
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,541
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 47
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: selected peptide
US-10-004-381-26

Query Match 66.0%; Score 31; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDEKTTGMRGSHVEGLAGELBQLRRLRLEHH 31
DB 1 MDEKTTGMRGSHVEGLAGELBQLRRLRLEHH 31

RESULT 12

US-10-004-381-29
Sequence 29, Application US/10004381
Publication No. US20020155578A1

GENERAL INFORMATION:
APPLICANT: SZOSTAK, JACK W.
APPLICANT: WILSON, DAVID S.
APPLICANT: KEEFE, ANTHONY D.
TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
FILE REFERENCE: 00786/388002
CURRENT APPLICATION NUMBER: US/10/004,381
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/244,541
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 29
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: selected peptide
US-10-004-381-29

Query Match 59.6%; Score 28; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. No. 9e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 ELEQLRLRLHHHPQGRPEPMMSGCKLKG 47
DB 2 ELEQLRLRLHHHPQGRPEPMMSGCKLKG 29

RESULT 13

US-10-004-381-28
Sequence 28, Application US/10004381
Publication No. US20020155578A1

GENERAL INFORMATION:
APPLICANT: SZOSTAK, JACK W.
APPLICANT: WILSON, DAVID S.
APPLICANT: KEEFE, ANTHONY D.
TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
FILE REFERENCE: 00786/388002
CURRENT APPLICATION NUMBER: US/10/004,381
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/244,541
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 89
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: selected peptide
US-10-004-381-28

Query Match 51.1%; Score 24; DB 14; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 EGIAGLEBQLRRLRHHHPQGRREP 38
DB 3 EGIAGLEBQLRRLRHHHPQGRREP 26

Search completed: February 6, 2004, 17:21:02
Job time : 35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 16:38:52 ; Search time 41 Seconds
(without alignments)
181.955 Million cell updates/sec

Title: US-10-004-381-25

Perfect score: 258

Sequence: 1 MDEKTTGRGHHVVEGLAGE.....LEHHQPGQREPMWGGCKLG 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits' satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
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- 12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
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- 19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	258	100.0	47	23	ABG67079
2	258	100.0	47	24	ABU57601
3	243	94.2	47	23	ABG67080
4	243	94.2	47	24	ABU57602
5	241	93.4	61	23	ABG67078
6	241	93.4	61	24	ABU57600
7	234	90.7	75	23	ABG67077
8	234	90.7	75	24	ABU57599
9	227	88.0	89	23	ABG67076
					Streptavidin-bindi
					Synthetic peptide
					Streptavidin-bindi
					Streptavidin-bindi
					Streptavidin-bindi
					Synthetic peptide
					Streptavidin-bindi
					Synthetic peptide
					Streptavidin-bindi

10	227	88.0	89	24	ABU57598	Synthetic peptide
11	214	82.9	101	23	ABG67075	Streptavidin-bindi
12	214	82.9	101	24	ABU57597	Streptavidin-bindi
13	211	81.8	101	23	ABG67073	Streptavidin-bindi
14	211	81.8	101	24	ABU57595	Streptavidin-bindi
15	208	80.6	38	23	ABG67087	Streptavidin-bindi
16	208	80.6	38	24	ABU57609	Streptavidin-bindi
17	208	80.6	426	23	ABG67091	Maltose-binding pr
18	208	80.6	426	24	ABU57613	Streptavidin-bindi
19	208	80.6	479	23	ABG67089	Maltose-binding pr
20	208	80.6	479	24	ABU57611	Streptavidin-bindi
21	199	77.1	39	23	ABG67081	Streptavidin-bindi
22	199	77.1	39	24	ABU57603	Synthetic peptide
23	152	58.9	29	23	ABG67083	Streptavidin-bindi
24	152	58.9	29	24	ABU57605	Synthetic peptide
25	133	51.6	89	23	ABG67082	Streptavidin-bindi
26	133	51.6	89	24	ABU57604	Synthetic peptide
27	94	36.4	44	23	ABG67086	Streptavidin-bindi
28	88	34.1	44	24	ABU57608	Streptavidin-nonbi
29	70	27.1	102	23	ABG67065	Streptavidin-bindi
30	70	27.1	102	24	ABU57587	Streptavidin-bindi
31	68	26.4	101	23	ABG67066	Streptavidin-bindi
32	68	26.4	101	24	ABU57588	Streptavidin-bindi
33	63	24.4	145	23	ABP09375	Human OREF protein
34	62	24.0	164	22	AAB63619	Human gastric canc
35	60.5	23.4	741	22	ABG25060	Novel human diagno
36	59.5	23.1	84	23	ABP34332	Human helicase-lik
37	59.5	23.1	342	21	AAB15903	E. coli proliferat
38	59.5	23.1	538	22	ABG25106	Novel human diagno
39	59	22.9	140	19	AAW40203	FRAP homolog. Cry
40	59	22.9	147	22	ABG54019	Human liver peptid
41	59	22.9	147	22	ABB39099	Peptide #6605 enco
42	59	22.9	147	22	ABB24009	Protein #6008 enco
43	59	22.9	147	22	AAM59751	Human brain expres
44	59	22.9	147	22	AAM72333	Human bone marrow
45	59	22.9	147	22	AAM19547	Peptide #5981 enco

ALIGNMENTS

RESULT 1
ABG67079
ID ABG67079 standard; Peptide; 47 AA.
XX
AC ABG67079;
XX
DT 24-SEP-2002 (first entry)
XX
DE Streptavidin-binding peptide SB19 truncation mutant #5.
XX
KW Streptavidin-binding peptide; mutant; mutein.
XX
OS Escherichia coli.
XX
PN WO200238580-A1.
XX
PD 16-MAY-2002.
XX
PF 31-OCT-2000; 2000WO-US41717.
XX
PR 31-OCT-2000; 2000WO-US41717.
XX
PA (GEHO) GEN HOSPITAL CORP.

XX Szostak JW, Wilson DS, Keefe AD;
XX WPI; 2002-500155/53.
XX
XX Novel peptide with high affinity for streptavidin, is expressed as part
XX of fusion protein to facilitate detection, quantitation and
XX purification of desired protein -
XX

PS Claim 9; Fig 5; 56pp; English.

XX The invention describes a peptide (I) which binds streptavidin with a

CC dissociation constant less than 10 μ M or 23 nM, where the amino acid

CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not

CC disulfide bonded or cyclised. A fusion protein comprising a protein of

CC interest covalently linked to (I) is useful for purifying a desired

CC protein from a sample by contacting the sample with streptavidin under

CC conditions that allow complex formation between the fusion protein and

CC the streptavidin, isolating the complex and recovering the fusion

CC protein, and thus purifying the desired protein from the sample. The

CC invention describes a method for producing a streptavidin-binding fusion

CC protein. This sequence represents a truncation mutant of the

CC streptavidin-binding peptide SB-19 isolated from *Escherichia coli* using a

XX method described in the specification.

SQ Sequence 47 AA;

Query Match 100.0%; Score 258; DB 23; Length 47;

Best Local Similarity 100.0%; Pred. No. 1.7e-28;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGRRGHVVEGLAGELEQLRLRLEHHHPQOREPMMSGGCKLG 47

DB 1 MDEKTTGRRGHVVEGLAGELEQLRLRLEHHHPQOREPMMSGGCKLG 47

RESULT 2

ABU57601

ID ABU57601 standard; Peptide; 47 AA.

AC ABU57601;

DT 09-APR-2003 (first entry)

DE Synthetic peptide SB19 C-terminal deletion mutant, C4.

KW Streptavidin-binding peptide; mRNA display; peptide library;

KW fusion protein; mutant; mutein; SB19.

OS Synthetic.

XX US2002155578-A1.

PN 24-OCT-2002.

PD 31-OCT-2001; 2001US-0004381.

XX 31-OCT-2000; 2000US-244541P.

PR (SZOS/) SZOSTAK J W.

PA (WILS/) WILSON D S.

PA (KEEF/) KEEFE A D.

XX Szostak JW, Wilson DS, Keefe AD;

PI WPI; 2003-182639/18.

DR Novel peptide which binds streptavidin with high affinity useful as

XX affinity tags for purifying fusion proteins containing proteins of

XX interest -

PS Claim 14; Fig 5; 36pp; English.

XX The invention relates to a peptide which binds streptavidin with a

CC dissociation constant less than 10 μ M, where the peptide is not

CC disulfide bonded or cyclised, or with a dissociation constant less than

CC 10 μ M, where the amino acid sequence of the peptide does not contain

CC an HPQ, HPM, HPN or HQP motif. The peptides are generated by the mRNA

CC display method to create a library of peptides. Also include are a

CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,

CC a fusion protein (and its encoding nucleic acid/vector) comprising a

XX protein of interest covalently linked to the streptavidin binding

CC peptide and detecting the presence of the fusion protein in a sample

CC using streptavidin or streptavidin-containing compounds. The fusion

CC protein (which comprises the desired protein of interest covalently

CC linked to the streptavidin binding peptide) is useful for purifying a

CC protein of interest from a sample, which involves expressing the

CC fusion protein in the sample, contacting the sample with streptavidin

CC under conditions that allow complex formation between the fusion protein

CC and the streptavidin, isolating the complex and recovering the fusion

CC protein, thereby purifying the protein of interest from the sample.

CC The present sequence is a mutated version of SB19, a streptavidin-binding

CC peptide of the invention. The mutants comprise 3 N-terminal deletions,

CC 3 C-terminal deletions and a truncated N-terminal peptide with point

XX mutations.

SQ Sequence 47 AA;

Query Match 100.0%; Score 258; DB 24; Length 47;

Best Local Similarity 100.0%; Pred. No. 1.7e-28;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGRRGHVVEGLAGELEQLRLRLEHHHPQOREPMMSGGCKLG 47

DB 1 MDEKTTGRRGHVVEGLAGELEQLRLRLEHHHPQOREPMMSGGCKLG 47

RESULT 3

ABG67080

ID ABG67080 standard; Peptide; 47 AA.

AC ABG67080;

DT 24-SEP-2002 (first entry)

DE Streptavidin-binding peptide SB19 truncation mutant #6.

KW Streptavidin-binding peptide; mutant; mutein.

XX *Escherichia coli*.

XX WO200238580-A1.

PN 16-MAY-2002.

PD 31-OCT-2000; 2000WO-US41717.

PF 31-OCT-2000; 2000WO-US41717.

PR (GEO) GEN HOSPITAL CORP.

XX Szostak JW, Wilson DS, Keefe AD;

PI WPI; 2002-500155/53.

DR Novel peptide with high affinity for streptavidin, is expressed as part

PT of fusion protein to facilitate detection, quantitation and

PT purification of desired protein -

XX Claim 9; Fig 5; 56pp; English.

XX The invention describes a peptide (I) which binds streptavidin with a

CC dissociation constant less than 10 μ M or 23 nM, where the amino acid

CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not

CC disulfide bonded or cyclised. A fusion protein comprising a protein of

CC interest covalently linked to (I) is useful for purifying a desired

CC protein from a sample by contacting the sample with streptavidin under

CC conditions that allow complex formation between the fusion protein and

CC the streptavidin, isolating the complex and recovering the fusion

CC protein, and thus purifying the desired protein from the sample. The

CC invention describes a method for producing a streptavidin-binding fusion

CC protein. This sequence represents a truncation mutant of the

CC streptavidin-binding peptide SB-19 isolated from *Escherichia coli* using a

XX method described in the specification.

SQ Sequence 47 AA;
 Query Match 94.2%; Score 243; DB 23; Length 47;
 Best Local Similarity 95.7%; Pred. No. 2.2e-26;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEKTTGRRGHVVEGLAGELEQLARLEHHHPQOREPMMSGGCKLG 47
 DB 1 MDEKTTGRRGHVVEGLAGELEQLARLEHHHPQOREPMMSGGCKLG 47

RESULT 4
 ABUS7602
 ID ABUS7602 standard; Peptide; 47 AA.
 XX
 AC ABUS7602;
 XX
 DT 09-APR-2003 (first entry)
 XX
 DE Streptavidin-binding synthetic peptide SB19 point mutant M1.
 XX
 KW Streptavidin-binding peptide; mRNA display; peptide library;
 KW fusion protein; mutant; mutein; SB19.
 XX
 OS Synthetic.
 XX
 XX US2002155578-A1.
 PN
 XX
 PD 24-OCT-2002.
 XX
 PF 31-OCT-2001; 2001US-0004381.
 XX
 PR 31-OCT-2000; 2000US-244541P.
 XX
 PA (SZOS/) SZOSTAK J W.
 PA (WILS/) WILSON D S.
 PA (KEEF/) KEEFE A D.
 XX
 PI Szostak JW, Wilson DS, Keefe AD;
 XX
 DR WPI; 2003-182639/18.
 XX
 PT Novel peptide which binds streptavidin with high affinity useful as
 PT affinity tags for purifying fusion proteins containing proteins of
 PT interest -
 XX
 PS Claim 14; Fig 5; 36pp; English.

CC The invention relates to a peptide which binds streptavidin with a
 CC dissociation constant less than 10 micro M, where the peptide is not
 CC disulphide bonded or cyclised, or with a dissociation constant less than
 CC 10 micro M, where the amino acid sequence of the peptide does not contain
 CC an HPQ, HPM, HPN or HQP motif. The peptides are generated by the mRNA
 CC display method to create a library of peptides. Also include are a
 CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
 CC a fusion protein (and its encoding nucleic acid/vector) comprising a
 CC protein of interest covalently linked to the streptavidin binding
 CC peptide and detecting the presence of the fusion protein in a sample
 CC using streptavidin or streptavidin-containing compounds. The fusion
 CC protein (which comprises the desired protein of interest covalently
 CC linked to the streptavidin binding peptide) is useful for purifying a
 CC protein of interest from a sample, which involves expressing the
 CC fusion protein in the sample, contacting the sample with streptavidin
 CC under conditions that allow complex formation between the fusion protein
 CC and the streptavidin, isolating the complex and recovering the fusion
 CC protein, thereby purifying the protein of interest from the sample.
 CC The present sequence is a mutated version of SB19, a streptavidin binding
 CC peptide of the invention. The mutants comprise 3 N-terminal deletions,
 CC 3 C-terminal deletions and a truncated N-terminal peptide with point
 CC mutations.

XX
 SQ Sequence 47 AA;

Query Match 94.2%; Score 243; DB 24; Length 47;
 Best Local Similarity 95.7%; Pred. No. 2.2e-26;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEKTTGRRGHVVEGLAGELEQLARLEHHHPQOREPMMSGGCKLG 47
 DB 1 MDEKTTGRRGHVVEGLAGELEQLARLEHHHPQOREPMMSGGCKLG 47

RESULT 5
 ABG67078
 ID ABG67078 standard; Peptide; 61 AA.
 XX
 AC ABG67078;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Streptavidin-binding peptide SB19 truncation mutant #4.
 XX
 KW Streptavidin-binding peptide; mutant; mutein.
 XX
 OS Escherichia coli.
 XX
 PW WO200238580-A1.
 XX
 PD 16-MAY-2002.
 XX
 PF 31-OCT-2000; 2000WO-US41717.
 XX
 PR 31-OCT-2000; 2000WO-US41717.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Szostak JW, Wilson DS, Keefe AD;
 XX
 DR WPI; 2002-500155/53.
 XX
 PT Novel peptide with high affinity for streptavidin, is expressed as part
 PT of fusion protein to facilitate detection, quantitation and
 PT purification of desired protein -
 XX
 PS Claim 9; Fig 5; 56pp; English.

CC The invention describes a peptide (I) which binds streptavidin with a
 CC dissociation constant less than 10 μM or 23 nM, where the amino acid
 CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not
 CC disulfide bonded or cyclised. A fusion protein comprising a protein of
 CC interest covalently linked to (I) is useful for purifying a desired
 CC protein from a sample by contacting the sample with streptavidin under
 CC conditions that allow complex formation between the fusion protein and
 CC the streptavidin, isolating the complex and recovering the fusion
 CC protein, and thus purifying the desired protein from the sample. The
 CC invention describes a method for producing a streptavidin-binding fusion
 CC protein. This sequence represents a truncation mutant of the
 CC streptavidin-binding peptide SB-19 isolated from Escherichia coli using a
 CC method described in the specification.

XX
 SQ Sequence 61 AA;

Query Match 93.4%; Score 241; DB 23; Length 61;
 Best Local Similarity 77.0%; Pred. No. 5.6e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MDEKTTGRRGHVVEGLAGELEQLARLEHHHPQOREP-----MMGGGCKL 46
 DB 1 MDEKTTGRRGHVVEGLAGELEQLARLEHHHPQOREP-----MMGGGCKL 60

QY 47 G 47
 DB 61 G 61

RESULT 6

ABUS7600
ID ABUS7600 standard; Peptide; 61 AA.
XX.
AC ABUS7600;
XX
XX 09-APR-2003 (first entry)
XX
XX Synthetic peptide SB19 C-terminal deletion mutant, C3.
XX
XX Streptavidin-binding peptide; mRNA display; peptide library;
KW fusion protein; mutant; mutein; SB19.
XX
XX Synthetic.
OS
XX US2002155578-A1.
XX
XX 24-OCT-2002.
PD
XX 31-OCT-2001; 2001US-0004381.
XX
XX 31-OCT-2000; 2000US-244541P.
PR
XX (SZOS/) SZOSTAK J W.
PA (WILS/) WILSON D S.
PA (KEEF/) KEEFE A D.
XX
XX Szostak JW, Wilson DS, Keefe AD;
PI
XX WPI; 2003-182639/18.
DR
XX Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
XX Claim 14; Fig 5; 36pp; English.
PS
XX The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPQ, HPM, or HQP motif. The peptides are generated by the mRNA
CC display method to create a library of peptides. Also include are a
CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
CC a fusion protein (and its encoding nucleic acid/vector) comprising a
CC protein of interest covalently linked to the streptavidin binding
CC peptide and detecting the presence of the fusion protein in a sample
CC using streptavidin or streptavidin-containing compounds. The fusion
CC protein (which comprises the desired protein of interest covalently
CC linked to the streptavidin binding peptide) is useful for purifying a
CC protein of interest from a sample, which involves expressing the
CC fusion protein in the sample, contacting the sample with streptavidin
CC under conditions that allow complex formation between the fusion protein
CC and the streptavidin, isolating the complex and recovering the fusion
CC protein, thereby purifying the protein of interest from the sample.
CC The present sequence is a mutated version of SB19, a streptavidin binding
CC peptide of the invention. The mutants comprise 3 N-terminal deletions,
CC 3 C-terminal deletions and a truncated N-terminal peptide with point
CC mutations.
XX
SQ Sequence 61 AA;
Query Match 93.4%; Score 241; DB 24; Length 61;
Best Local Similarity 77.0%; Pred. No. 5.6e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
OY 1 MDEKTTGRRGHHVVEGLAGELQLRRLRLEHHHPQGOREP-----MMSGGCKL 46
DB 1 MDEKTTGRRGHHVVEGLAGELQLRRLRLEHHHPQGOREP-----MMSGGCKL 60
OY 47 G 47
DB 61 G 61

RESULT 7
ABG67077
ID ABG67077 standard; Peptide; 75 AA.
XX
XX AC ABG67077;
XX
XX 24-SEP-2002 (first entry)
XX
XX Streptavidin-binding peptide SB19 truncation mutant #3.
DE Streptavidin-binding peptide; mutant; mutein.
KW Streptavidin-binding peptide; mutant; mutein.
XX
XX Escherichia coli.
OS
XX WO200238580-A1.
XX
XX 16-MAY-2002.
PD
XX 31-OCT-2000; 2000WO-US41717.
XX
XX 31-OCT-2000; 2000WO-US41717.
PR
XX (GEHO) GEN HOSPITAL CORP.
PA
XX Szostak JW, Wilson DS, Keefe AD;
PI
XX WPI; 2002-500155/53.
DR
XX Novel peptide with high affinity for streptavidin, is expressed as part
PT of fusion protein to facilitate detection, quantitation and
PT purification of desired protein -
XX
XX Claim 9; Fig 5; 56pp; English.
PS
XX The invention describes a peptide (I) which binds streptavidin with a
CC dissociation constant less than 10 muM or 23 nM, where the amino acid
CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not
CC disulfide bonded or cyclised. A fusion protein comprising a protein of
CC interest covalently linked to (I) is useful for purifying a desired
CC protein from a sample by contacting the sample with streptavidin under
CC conditions that allow complex formation between the fusion protein and
CC the streptavidin, isolating the complex and recovering the fusion
CC protein, and thus purifying the desired protein from the sample. The
CC invention describes a method for producing a streptavidin-binding fusion
CC protein. This sequence represents a truncation mutant of the
CC streptavidin-binding peptide SB-19 isolated from Escherichia coli using a
CC method described in the specification.
XX
SQ Sequence 75 AA;
Query Match 90.7%; Score 234; DB 23; Length 75;
Best Local Similarity 62.7%; Pred. No. 6.7e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 28; Gaps 1;
OY 1 MDEKTTGRRGHHVVEGLAGELQLRRLRLEHHHPQGOREP----- 38
DB 1 MDEKTTGRRGHHVVEGLAGELQLRRLRLEHHHPQGOREP----- 38
OY 39 -----MMSGGCKLG 47
DB 61 LLDPVEMMSGGCKLG 75
RESULT 8
ABUS7599
ID ABUS7599 standard; Peptide; 75 AA.
XX
XX AC ABUS7599;
XX
XX 09-APR-2003 (first entry)
DE Synthetic peptide SB19 C-terminal deletion mutant, C2.

XX Streptavidin-binding peptide; mRNA display; peptide library;
KW fusion protein; mutant; mutein; SB19.
XX Synthetic.
OS
XX US2002155578-A1.
PN
XX 24-OCT-2002.
XX
XX 31-OCT-2001; 2001US-0004381.
PF
XX 31-OCT-2000; 2000US-244541P.
PR
XX (SZOS/) SZOSTAK J W.
PA (WILS/) WILSON D S.
PA (KEEF/) KEEFE A D.
XX
PI Szostak JW, Wilson DS, Keefe AD;
XX
XX WPI; 2003-182639/18.
DR
XX Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
XX Claim 14; Fig 5; 36pp; English.
PS
XX The invention relates to a peptide which binds streptavidin with a
XX dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPQ, HPM, or HQP motif. The peptides are generated by the mRNA
CC display method to create a library of peptides. Also include are a
CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
CC a fusion protein (and its encoding nucleic acid/vector) comprising a
CC protein of interest covalently linked to the streptavidin binding
CC peptide and detecting the presence of the fusion protein in a sample
CC using streptavidin or streptavidin-containing compounds. The fusion
CC protein (which comprises the desired protein) of interest covalently
CC linked to the streptavidin binding peptide) is useful for purifying a
CC protein of interest from a sample, which involves expressing the
CC fusion protein in the sample, contacting the sample with streptavidin
CC under conditions that allow complex formation between the fusion protein
CC and the streptavidin, isolating the complex and recovering the fusion
CC protein, thereby purifying the protein of interest from the sample.
CC The present sequence is a mutated version of SB19, a streptavidin binding
CC peptide of the invention. The mutants comprise 3 N-terminal deletions,
CC 3 C-terminal deletions and a truncated N-terminal peptide with point
CC mutations.
XX
XX Sequence 75 AA;
SQ
Query Match 90.7%; Score 234; DB 24; Length 75;
Best Local Similarity 62.7%; Pred. No. 6.7e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 28; Gaps 1;
QY 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLHHHPQOGREP----- 38
DB 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLHHHPQOGREP----- 60
QY 39 -----MMSGGCKLG 47
DB 61 LLDPVEMMSGCKLG 75
RESULT 9
ABG67076
ID *ABG67076 standard; Peptide; 89 AA.
XX
AC ABG67076;
XX
DT 24-SEP-2002 (first entry)

XX Streptavidin-binding peptide SB19 truncation mutant #2.
DE
XX Streptavidin-binding peptide; mutant; mutein.
KW
XX Escherichia coli.
OS
XX WO200238580-A1.
PN
XX 16-MAY-2002.
XX
XX 31-OCT-2000; 2000WO-US41717.
PF
XX 31-OCT-2000; 2000WO-US41717.
PR
XX (GEOH) GEN HOSPITAL CORP.
PA
XX
PI Szostak JW, Wilson DS, Keefe AD;
XX
XX WPI; 2002-500155/53.
DR
XX Novel peptide with high affinity for streptavidin, is expressed as part
PT of fusion protein to facilitate detection, quantitation and
PT purification of desired protein -
XX
XX Claim 9; Fig 5; 56pp; English.
PS
XX The invention describes a peptide (I) which binds streptavidin with a
CC dissociation constant less than 10 mM or 23 nM, where the amino acid
CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not
CC disulphide bonded or cyclised. A fusion protein comprising a protein of
CC interest covalently linked to (I) is useful for purifying a desired
CC protein from a sample by contacting the sample with streptavidin under
CC conditions that allow complex formation between the fusion protein and
CC the streptavidin, isolating the complex and recovering the fusion
CC protein, and thus purifying the desired protein from the sample. The
CC invention describes a method for producing a streptavidin-binding fusion
CC protein. This sequence represents a truncation mutant of the
CC streptavidin-binding peptide SB-19 isolated from Escherichia coli using a
CC method described in the specification.
XX
XX Sequence 89 AA;
SQ
Query Match 88.0%; Score 227; DB 23; Length 89;
Best Local Similarity 52.8%; Pred. No. 7.7e-24;
Matches 47; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
QY 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLHHHPQOGREP----- 38
DB 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLHHHPQOGREP----- 60
QY 39 -----MMSGGCKLG 47
DB 61 LLDPVEKLLTDWFKFKFNVMMSGCKLG 89
RESULT 10
ABU57598
ID ABU57598 standard; Peptide; 89 AA.
XX
AC ABU57598;
XX
XX 09-APR-2003 (first entry)
DT
XX
DE Synthetic peptide SB19 C-terminal deletion mutant, C1.
XX
KW Streptavidin-binding peptide; mRNA display; peptide library;
KW fusion protein; mutant; mutein; SB19.
XX
OS Synthetic.
XX
PN US2002155578-A1.
XX

PD *24-OCT-2002.
XX
PF 31-OCT-2001; 2001US-0004381.
XX
PR 31-OCT-2000; 2000US-244541P.
XX
PA (SZOS/) SZOSTAK J W.
PA (WILS/) WILSON D S.
PA (KEEF/) KEEFE A D.
XX
PI Szostak JW, Wilson DS, Keefe AD;
XX
DR WPI; 2003-182639/18.
XX
XX Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
PS Claim 14; Fig 5; 36pp; English.
XX
CC The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPQ, HPM, or HQP motif. The peptides are generated by the mRNA
CC display method to create a library of peptides. Also include are a
CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
CC a fusion protein (and its encoding nucleic acid/vector) comprising a
CC protein of interest covalently linked to the streptavidin binding
CC peptide and detecting the presence of the fusion protein in a sample
CC using streptavidin or streptavidin-containing compounds. The fusion
CC protein (which comprises the desired protein of interest covalently
CC linked to the streptavidin binding peptide) is useful for purifying a
CC protein of interest from a sample, which involves expressing the
CC fusion protein in the sample, contacting the sample with streptavidin
CC under conditions that allow complex formation between the fusion protein
CC and the streptavidin, isolating the complex and recovering the fusion
CC protein, thereby purifying the protein of interest from the sample.
CC The present sequence is a mutated version of SB19, a streptavidin binding
CC peptide of the invention. The mutants comprise 3 N-terminal deletions,
CC 3 C-terminal deletions and a truncated N-terminal peptide with point
CC mutations.
XX
SQ Sequence 89 AA;
Query Match 88.0%; Score 227; DB 24; Length 89;
Best Local Similarity 52.8%; Pred. No. 7.7e-24;
Matches 47; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
QY 1 MDEKTTGRRGGHVVEGLAGELEQLRLARLEHHHPQGGREP----- 38
DB 1 MDEKTTGRRGGHVVEGLAGELEQLRLARLEHHHPQGGREPVLQVEDVDGLVQDLHGTVAG 60
QY 39 -----MMSGGCKLG 47
DB 61 LLDPEVKLLTDWFKFKFNKNSDKCKMTFYLEMYDWSGGCKLG 89
RESULT 11
ABG67075
ID ABG67075 standard; Peptide; 101 AA.
XX
AC ABG67075;
XX
DT 24-SEP-2002 (first entry)
XX
DE Streptavidin-binding peptide SB19 truncation mutant #1.
XX
KW Streptavidin-binding peptide; mutant; mutein.
XX
OS Escherichia coli.
OS Synthetic.
XX

PN WO200238580-A1.
XX
PD 16-MAY-2002.
XX
PF 31-OCT-2000; 2000WO-US41717.
XX
PR 31-OCT-2000; 2000WO-US41717.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Szostak JW, Wilson DS, Keefe AD;
XX
DR WPI; 2002-500155/53.
XX
XX Novel peptide with high affinity for streptavidin, is expressed as part
PT of fusion protein to facilitate detection, quantitation and
PT purification of desired protein -
XX
PS Claim 9; Fig 5; 56pp; English.
XX
CC The invention describes a peptide (I) which binds streptavidin with a
CC dissociation constant less than 10 mM or 23 nM, where the amino acid
CC sequence of (I) does not contain an HPQ, HPM, or HQP motif, is not
CC disulphide bonded or cyclised. A fusion protein comprising a protein of
CC interest covalently linked to (I) is useful for purifying a desired
CC protein from a sample by contacting the sample with streptavidin under
CC conditions that allow complex formation between the fusion protein and
CC the streptavidin, isolating the complex and recovering the fusion
CC protein, and thus purifying the desired protein from the sample. The
CC invention describes a method for producing a streptavidin-binding fusion
CC protein. This sequence represents a truncation mutant of the
CC streptavidin-binding peptide SB-19 isolated from Escherichia coli using a
CC method described in the specification.
XX
SQ Sequence 101 AA;
Query Match 82.9%; Score 214; DB 23; Length 101;
Best Local Similarity 44.6%; Pred. No. 5.8e-22;
Matches 45; Conservative 2; Mismatches 0; Indels 54; Gaps 1;
QY 1 MDEKTTGRRGGHVVEGLAGELEQLRLARLEHHHPQGGREPMM----- 40
DB 1 MDEKTTGRRGGHVVEGLAGELEQLRLARLEHHHPQGGREPVLQVEDVDGLVQDLHGTVAG 60
QY 41 -----SGGCKLG 47
DB 61 LLDPEVKLLTDWFKFKFNKNSDKCKMTFYLEMYDWSGGCKLG 101
RESULT 12
ABUS7597
ID ABUS7597 standard; Peptide; 101 AA.
XX
AC ABUS7597;
XX
DT 09-APR-2003 (first entry)
XX
DE Streptavidin-binding synthetic peptide SB19 full length peptide.
XX
KW Streptavidin-binding peptide; mRNA display; peptide library;
KW fusion protein.
XX
OS Synthetic.
XX
PN US2002155578-A1.
XX
PD 24-OCT-2002.
XX
PF 31-OCT-2001; 2001US-0004381.
XX
PR 31-OCT-2000; 2000US-244541P.
XX
PA (SZOS/) SZOSTAK J W.
XX

PA (WILS/) WILSON D S.
XX (KEEF/) KEEFE A D.
PI Szostak JW, Wilson DS, Keefe AD;
XX WPI; 2003-182639/18.
DR
XX Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
PS Claim 14; Fig 5; 36pp; English.
XX
CC The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPQ, HPM, HPN or HQP motif. The peptides are generated by the mRNA
CC display method to create a library of peptides. Also include are a
CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
CC a fusion protein (and its encoding nucleic acid/vector) comprising a
CC protein of interest covalently linked to the streptavidin binding
CC peptide and detecting the presence of the fusion protein in a sample
CC using streptavidin or streptavidin-containing compounds. The fusion
CC protein (which comprises the desired protein of interest covalently
CC linked to the streptavidin binding peptide) is useful for purifying a
CC protein of interest from a sample, which involves expressing the
CC fusion protein in the sample, contacting the sample with streptavidin
CC under conditions that allow complex formation between the fusion protein
CC and the streptavidin, isolating the complex and recovering the fusion
CC protein, thereby purifying the protein of interest from the sample.
CC The present sequence is a streptavidin binding peptide of the invention.
XX
SQ Sequence. 101 AA;

Query Match 82.9%; Score 214; DB 24; Length 101;
Best Local Similarity 44.6%; Pred. No. 5.8e-22;
Matches 45; Conservative 2; Mismatches 0; Indels 54; Gaps 1;

QY 1 MDEKTTGRRGGHVVEGLAGELEQLRLEHHHPQOREPMM-----SGGCKLG 47
DB 1 MDEKTTGRRGGHVVEGLAGELEQLRLEHHHPQOREPLVQVEVDVDEGLVODLHGTVAG 60
QY 41 -----SGGCKLG 47
DB 61 LLDPEKLLTDWFKFKVSKDKCTFFYLEWYDWSGGCKLG 101

RESULT 13
ABG67073
ID ABG67073 standard; Peptide; 101 AA.
XX
AC ABG67073;
XX
DT 24-SEP-2002 (first entry)
XX
DE Streptavidin-binding peptide SB19.
XX
KW Streptavidin-binding peptide.
XX
OS Escherichia coli.
XX
PN WO200238580-A1.
XX
PD 16-MAY-2002.
XX
PF 31-OCT-2000; 2000WO-US41717.
XX
PR 31-OCT-2000; 2000WO-US41717.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Szostak JW, Wilson DS, Keefe AD;

XX WPI; 2002-500155/53.
XX Novel peptide with high affinity for streptavidin, is expressed as part
PT of fusion protein to facilitate detection, quantitation and
PT purification of desired protein -
XX
PS Claim 9; Fig 3; 56pp; English.
XX
CC The invention describes a peptide (I) which binds streptavidin with a
CC dissociation constant less than 10 mM or 23 nM, where the amino acid
CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not
CC disulphide bonded or cyclised. A fusion protein comprising a protein of
CC interest covalently linked to (I) is useful for purifying a desired
CC protein from a sample by contacting the sample with streptavidin under
CC conditions that allow complex formation between the fusion protein and
CC the streptavidin, isolating the complex and recovering the fusion
CC protein, and thus purifying the desired protein from the sample. The
CC invention describes a method for producing a streptavidin-binding fusion
CC protein. This sequence represents a streptavidin-binding peptide isolated
CC from Escherichia coli using a method described in the specification.
XX
SQ Sequence 101 AA;

Query Match 81.8%; Score 211; DB 23; Length 101;
Best Local Similarity 95.0%; Pred. No. 1.5e-21;
Matches 38; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGRRGGHVVEGLAGELEQLRLEHHHPQOREPMM 40
DB 1 MDEKTTGRRGGHVVEGLAGELEQLRLEHHHPQOREPLV 40

RESULT 14
ABU57595
ID ABU57595 standard; Peptide; 101 AA.
XX
AC ABU57595;
XX
DT 09-APR-2003 (first entry)
XX
DE Streptavidin-binding synthetic peptide SB19.
XX
KW Streptavidin-binding peptide; mRNA display; peptide library;
XX fusion protein.
XX
OS Synthetic.
XX
PN US2002155578-A1.
XX
PD 24-OCT-2002.
XX
PF 31-OCT-2001; 2001US-0004381.
XX
PR 31-OCT-2000; 2000US-244541P.
XX
PA (SZOS/) SZOSTAK J W.
XX (WILS/) WILSON D S.
PA (KEEF/) KEEFE A D.
XX
PI Szostak JW, Wilson DS, Keefe AD;
XX
DR WPI; 2003-182639/18.
XX
PT Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
PS Claim 14; Fig 3; 36pp; English.
XX
CC The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than

10 micro M, where the amino acid sequence of the peptide does not contain an HPQ, HPM, HPN or HQP motif. The peptides are generated by the mRNA display method to create a library of peptides. Also include are a nucleic acid encoding the peptide, a vector comprising the nucleic acid, a fusion protein (and its encoding nucleic acid/vector) comprising a protein of interest covalently linked to the streptavidin binding peptide and detecting the presence of the fusion protein in a sample using streptavidin or streptavidin-containing compounds. The fusion protein (which comprises the desired protein) of interest covalently linked to the streptavidin binding peptide) is useful for purifying a protein of interest from a sample, which involves expressing the fusion protein in the sample, contacting the sample with streptavidin under conditions that allow complex formation between the fusion protein and the streptavidin, isolating the complex and recovering the fusion protein, thereby purifying the protein of interest from the sample. The present sequence is a streptavidin binding peptide of the invention.

SQ Sequence 101 AA;

Query Match 81.8%; Score 211; DB 24; Length 101;
Best Local Similarity 95.0%; Pred. No. 1.5e-21;
Matches 38; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLEHHHPQGOREPMM 40
|||||
Db 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLEHHHPQGOREPLV 40

RESULT 15

ABG67087
ID ABG67087 standard; Peptide; 38 AA.

AC ABG67087;

DT 24-SEP-2002 (first entry)

DE Streptavidin-binding peptide and affinity tag.

KW Streptavidin-binding peptide.

OS Synthetic.

PN WO200238580-A1.

XX 16-MAY-2002.

PF 31-OCT-2000; 2000WO-US41717.

PR 31-OCT-2000; 2000WO-US41717.

PA (GEO) GEN HOSPITAL CORP.

PI Szostak JW, Wilson DS, Keefe AD;

XX WPI; 2002-500155/53.

PT Novel peptide with high affinity for streptavidin, is expressed as part of fusion protein to facilitate detection, quantitation and purification of desired protein

PS Claim 13; Fig 7A; 56pp; English.

XX The invention describes a peptide (I) which binds streptavidin with a dissociation constant less than 10 μM or 23 nM, where the amino acid sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not disulfide bonded or cyclised. A fusion protein comprising a protein of interest covalently linked to (I) is useful for purifying a desired protein from a sample by contacting the sample with streptavidin under conditions that allow complex formation between the fusion protein and the streptavidin, isolating the complex and recovering the fusion protein, and thus purifying the desired protein from the sample. The invention describes a method for producing a streptavidin-binding fusion protein. This sequence represents a streptavidin-binding peptide used in

CC the creation of streptavidin-binding DNA-tagged peptide described in the invention.

XX SQ Sequence 38 AA;

Query Match 80.6%; Score 208; DB 23; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLEHHHPQGOREP 38
|||||
Db 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLEHHHPQGOREP 38

Search completed: February 6, 2004, 16:40:31
Job time : 61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 6, 2004, 17:14:57 ; Search time 41 Seconds

(without alignments)

181.955 Million cell updates/sec

Title: US-10-004-381-25

Perfect score: 47

Sequence: 1 MDEKTTGWRGHVVEGLAGE.....LEHHPQGRPEPMSSGGCKLG 47

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 10

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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2: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1981.DAT.*
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6: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1992.DAT.*
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15: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	47	23	ABG67079
2	47	100.0	47	24	ABU57601
3	38	80.9	38	23	ABG67087
4	38	80.9	38	24	ABU57609
5	38	80.9	61	23	ABG67078
6	38	80.9	61	24	ABU57600
7	38	80.9	75	23	ABG67077
8	38	80.9	75	24	ABU57599
9	38	80.9	89	23	ABG67076

10	38	80.9	89	24	ABU57598	Synthetic peptide
11	38	80.9	101	23	ABG67073	Streptavidin-bindi
12	38	80.9	101	23	ABG67075	Streptavidin-bindi
13	38	80.9	101	24	ABU57595	Streptavidin-bindi
14	38	80.9	101	24	ABU57597	Streptavidin-bindi
15	38	80.9	426	23	ABG67091	Maltose-binding pr
16	38	80.9	426	23	ABG67613	Streptavidin-bindi
17	38	80.9	479	23	ABG67089	Maltose-binding pr
18	38	80.9	479	24	ABU57611	Streptavidin-bindi
19	37	78.7	39	23	ABG67081	Streptavidin-bindi
20	37	78.7	39	24	ABU57603	Synthetic peptide
21	31	66.0	47	23	ABG67080	Streptavidin-bindi
22	31	66.0	47	24	ABU57602	Streptavidin-bindi
23	28	59.6	29	23	ABG67083	Streptavidin-bindi
24	28	59.6	29	24	ABU57605	Synthetic peptide
25	24	51.1	89	23	ABG67082	Streptavidin-bindi
26	24	51.1	89	24	ABU57604	Synthetic peptide

ALIGNMENTS

RESULT 1

ABG67079

ID ABG67079 standard; Peptide; 47 AA.

XX

AC ABG67079;

XX

DT 24-SEP-2002 (first entry)

XX

DE Streptavidin-binding peptide SB19 truncation mutant #5.

XX

KW Streptavidin-binding peptide; mutant; mutein.

XX

OS Escherichia coli.

XX

PN WO200238580-A1.

XX

PD 16-MAY-2002.

XX

PF 31-OCT-2000; 2000WO-US41717.

XX

PR 31-OCT-2000; 2000WO-US41717.

XX

PA (GEO) GEN HOSPITAL CORP.

XX

PI Szostak JW, Wilson DS, Keefe AD;

XX

DR WPI; 2002-500155/53.

XX

PT Novel peptide with high affinity for streptavidin, is expressed as part of fusion protein to facilitate detection, quantitation and purification of desired protein

XX

PS Claim 9; Fig 5; 56pp; English.

XX

CC The invention describes a peptide (I) which binds streptavidin with a dissociation constant less than 10 mM or 23 nM, where the amino acid sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not disulfide bonded or cyclised. A fusion protein comprising a protein of interest covalently linked to (I) is useful for purifying a desired protein from a sample by contacting the sample with streptavidin under conditions that allow complex formation between the fusion protein and the streptavidin, isolating the complex and recovering the fusion protein, and thus purifying the desired protein from the sample. The invention describes a method for producing a streptavidin-binding fusion protein. This sequence represents a truncation mutant of the streptavidin-binding peptide SB-19 isolated from Escherichia coli using a method described in the specification.

XX

SQ Sequence 47 AA;

Query Match 100.0%; Score 47; DB 23; Length 47;

Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGRRGHVVEGLAGELEQLRLEHHHPQOREPMMSGCKLG 47
DB 1 MDEKTTGRRGHVVEGLAGELEQLRLEHHHPQOREPMMSGCKLG 47

RESULT 2
ABUS7601
ID ABUS7601 standard; Peptide; 47 AA.
AC ABUS7601;
DT 09-APR-2003 (first entry)
XX
DE Synthetic peptide SB19 C-terminal deletion mutant, C4.
KW Streptavidin-binding peptide; mRNA display; peptide library;
KW fusion protein; mutant; mutein; SB19.
XX
OS Synthetic.
XX
PN US2002155578-A1.
XX
PD 24-OCT-2002.
XX
PF 31-OCT-2001; 2001US-0004381.
XX
PR 31-OCT-2000; 2000US-244541P.
XX
PA (SZOS/) SZOSTAK J W.
PA (WILS/) WILSON D S.
PA (KEBF/) KEEFE A D.
XX
PI Szostak JW, Wilson DS, Keefe AD;
DR WPI; 2003-182639/18.
XX
PT Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -

Claim 14; Fig 5; 36pp; English.
XX
CC The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPQ, HPM, HPN or HQP motif. The peptides are generated by the mRNA
CC display method to create a library of peptides. Also include are a
CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
CC a fusion protein (and its encoding nucleic acid/vector) comprising a
CC peptide and detecting the presence of the fusion protein in a sample
CC using streptavidin or streptavidin-containing compounds. The fusion
CC protein (which comprises the desired protein of interest covalently
CC linked to the streptavidin binding peptide) is useful for purifying a
CC protein of interest from a sample, which involves expressing the
CC fusion protein in the sample, contacting the sample with streptavidin
CC under conditions that allow complex formation between the fusion protein
CC and the streptavidin, isolating the complex and recovering the fusion
CC protein, thereby purifying the protein of interest from the sample.
CC The present sequence is a mutated version of SB19, a streptavidin binding
CC peptide of the invention. The mutants comprise 3 N-terminal deletions,
CC 3 C-terminal deletions and a truncated N-terminal peptide with point
CC mutations.
XX
SQ Sequence 47 AA;

Query Match 100.0%; Score 47; DB 24; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGRRGHVVEGLAGELEQLRLEHHHPQOREPMMSGCKLG 47
DB 1 MDEKTTGRRGHVVEGLAGELEQLRLEHHHPQOREPMMSGCKLG 47

QY 1 MDEKTTGRRGHVVEGLAGELEQLRLEHHHPQOREPMMSGCKLG 47
DB 1 MDEKTTGRRGHVVEGLAGELEQLRLEHHHPQOREPMMSGCKLG 47

RESULT 3
ABG67087
ID ABG67087 standard; Peptide; 38 AA.
XX
AC ABG67087;
DT 24-SEP-2002 (first entry)
XX
DE Streptavidin-binding peptide and affinity tag.
XX
KW Streptavidin-binding peptide.
XX
OS Synthetic.
XX
PN WO200238580-A1.
XX
PD 16-MAY-2002.
XX
PF 31-OCT-2000; 2000WO-US41717.
XX
PR 31-OCT-2000; 2000WO-US41717.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Szostak JW, Wilson DS, Keefe AD;
DR WPI; 2002-500155/53.
XX
PT Novel peptide with high affinity for streptavidin, is expressed as part
PT of fusion protein to facilitate detection, quantitation and
PT purification of desired protein -
XX
PS Claim 13; Fig 7A; 56pp; English.
XX

The invention describes a peptide (I) which binds streptavidin with a
dissociation constant less than 10 μM or 23 nM, where the amino acid
sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not
disulfide bonded or cyclised. A fusion protein comprising a protein of
interest covalently linked to (I) is useful for purifying a desired
protein from a sample by contacting the sample with streptavidin under
conditions that allow complex formation between the fusion protein and
the streptavidin, isolating the complex and recovering the fusion
protein, and thus purifying the desired protein from the sample. The
invention describes a method for producing a streptavidin-binding fusion
protein. This sequence represents a streptavidin-binding peptide used in
the creation of streptavidin-binding DNA-tagged peptide described in the
invention.

Query Match 80.9%; Score 38; DB 23; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.1e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEKTTGRRGHVVEGLAGELEQLRLEHHHPQOREP 38
DB 1 MDEKTTGRRGHVVEGLAGELEQLRLEHHHPQOREP 38

RESULT 4
ABUS7609
ID ABUS7609 standard; Peptide; 38 AA.
XX
AC ABUS7609;
XX
DT 09-APR-2003 (first entry)
XX

DE Streptavidin-binding synthetic peptide SB19 C4 N-terminal affinity tag.
 XX
 KW Streptavidin-binding peptide; mRNA display; peptide library;
 XX fusion protein; SB19.
 KW
 OS Synthetic.
 XX
 PN US2002155578-A1.
 XX
 PD 24-OCT-2002.
 XX
 XX 31-OCT-2001; 2001US-0004381.
 XX
 PR 31-OCT-2000; 2000US-244541P.
 XX
 XX (SZOS/) SZOSTAK J W.
 PA (WILS/) WILSON D S.
 PA (KEEF/) KEEFE A D.
 XX
 PI Szostak JW, Wilson DS, Keefe AD;
 XX
 XX WPI; 2003-182639/18.
 XX
 XX Novel peptide which binds streptavidin with high affinity useful as
 PT affinity tags for purifying fusion proteins containing proteins of
 PT interest -
 XX
 PS Claim 14; Fig 7A; 36pp; English.
 XX
 CC The invention relates to a peptide which binds streptavidin with a
 CC dissociation constant less than 10 micro M, where the peptide is not
 CC disulphide bonded or cyclised, or with a dissociation constant less than
 CC 10 micro M, where the amino acid sequence of the peptide does not contain
 CC an HPQ, HPM, HPN or HQP motif. The peptides are generated by the mRNA
 CC display method to create a library of peptides. Also include are a
 CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
 CC a fusion protein (and its encoding nucleic acid/vector) comprising a
 CC protein of interest covalently linked to the streptavidin binding
 CC peptide and detecting the presence of the fusion protein in a sample
 CC using streptavidin or streptavidin-containing compounds. The fusion
 CC protein (which comprises the desired protein of interest covalently
 CC linked to the streptavidin binding peptide) is useful for purifying a
 CC protein of interest from a sample, which involves expressing the
 CC fusion protein in the sample, contacting the sample with streptavidin
 CC under conditions that allow complex formation between the fusion protein
 CC and the streptavidin, isolating the complex and recovering the fusion
 CC protein, thereby purifying the protein of interest from the sample.
 CC The present sequence is streptavidin binding peptide SB19.
 CC N-terminus, used as an affinity tag to purify fusion proteins.
 XX
 SQ Sequence 38 AA;
 Query Match 80.9%; Score 38; DB 24; Length 38;
 Best Local Similarity 100.0%; Pred. No. 4.1e-33;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDEKTTGRRGHVVEGLAGELEQLRLARLHHHPQGOREP 38
 DB 1 MDEKTTGRRGHVVEGLAGELEQLRLARLHHHPQGOREP 38
 RESULT 5
 ABG67078
 ID ABG67078 standard; Peptide; 61 AA.
 XX
 AC ABG67078;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Streptavidin-binding peptide SB19 truncation mutant #4.
 XX
 KW Streptavidin-binding peptide; mutant; mutein.
 XX

OS Escherichia coli.
 XX
 PN WO200238580-A1.
 XX
 PD 16-MAY-2002.
 XX
 PF 31-OCT-2000; 2000WO-US41717.
 XX
 PR 31-OCT-2000; 2000WO-US41717.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Szostak JW, Wilson DS, Keefe AD;
 XX
 XX WPI; 2002-500155/53.
 XX
 DR Novel peptide with high affinity for streptavidin, is expressed as part
 PT of fusion protein to facilitate detection, quantitation and
 PT purification of desired protein -
 XX
 PS Claim 9; Fig 5; 56pp; English.
 XX
 CC The invention describes a peptide (I) which binds streptavidin with a
 CC dissociation constant less than 10 muM or 23 nM, where the amino acid
 CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not
 CC disulfide bonded or cyclised. A fusion protein comprising a protein of
 CC interest covalently linked to (I) is useful for purifying a desired
 CC protein from a sample by contacting the sample with streptavidin under
 CC conditions that allow complex formation between the fusion protein and
 CC the streptavidin, isolating the complex and recovering the fusion
 CC protein, and thus purifying the desired protein from the sample. The
 CC invention describes a method for producing a streptavidin-binding fusion
 CC protein. This sequence represents a truncation mutant of the
 CC streptavidin-binding peptide SB-19 isolated from Escherichia coli using a
 CC method described in the specification.
 XX
 SQ Sequence 61 AA;
 Query Match 80.9%; Score 38; DB 23; Length 61;
 Best Local Similarity 100.0%; Pred. No. 6.3e-33;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDEKTTGRRGHVVEGLAGELEQLRLARLHHHPQGOREP 38
 DB 1 MDEKTTGRRGHVVEGLAGELEQLRLARLHHHPQGOREP 38
 RESULT 6
 ABUS7600
 ID ABUS7600 standard; Peptide; 61 AA.
 XX
 AC ABUS7600;
 XX
 DT 09-APR-2003 (first entry)
 XX
 DE Synthetic peptide SB19 C-terminal deletion mutant, C3.
 XX
 KW Streptavidin-binding peptide; mRNA display; peptide library;
 KW fusion protein; mutant; mutein; SB19.
 XX
 OS Synthetic.
 XX
 PN US2002155578-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 31-OCT-2001; 2001US-0004381.
 XX
 PR 31-OCT-2000; 2000US-244541P.
 XX
 XX (SZOS/) SZOSTAK J W.
 PA (WILS/) WILSON D S.
 PA (KEEF/) KEEFE A D.

XX Szostak JW, Wilson DS, Keefe AD;
PI WPI; 2003-182639/18.
DR
XX
XX Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
XX Claim 14; Fig 5; 36pp; English.
XX
XX The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPQ, HPM, HPN or HQP motif. The peptides are generated by the mRNA
CC display method to create a library of peptides. Also include are a
CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
CC a fusion protein (and its encoding nucleic acid/vector) comprising a
CC protein of interest covalently linked to the streptavidin binding
CC peptide and detecting the presence of the fusion protein in a sample
CC using streptavidin or streptavidin-containing compounds. The fusion
CC protein (which comprises the desired protein of interest covalently
CC linked to the streptavidin binding peptide) is useful for purifying a
CC protein of interest from a sample, which involves expressing the
CC fusion protein in the sample, contacting the sample with streptavidin
CC under conditions that allow complex formation between the fusion protein
CC and the streptavidin, isolating the complex and recovering the fusion
CC protein, thereby purifying the protein of interest from the sample.
CC The present sequence is a mutated version of SB19, a streptavidin binding
CC peptide of the invention. The mutants comprise 3 N-terminal deletions,
CC 3 C-terminal deletions and a truncated N-terminal peptide with point
CC mutations.
XX
XX SQ Sequence 61 AA;
Query Match 80.9%; Score 38; DB 24; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.3e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDEKTTGWRGHHVVEGLAGELEQLRLARLEHHHPQGOREP 38
DB 1 MDEKTTGWRGHHVVEGLAGELEQLRLARLEHHHPQGOREP 38
RESULT 7
ABG67077
ID ABG67077 standard; Peptide; 75 AA.
XX
XX AC ABG67077;
XX
XX DT 24-SEP-2002 (first entry)
XX
XX DE Streptavidin-binding peptide SB19 truncation mutant #3.
XX
XX KW Streptavidin-binding peptide; mutant; mutein.
XX
XX OS Escherichia coli.
XX
XX PN WO200238580-A1.
XX
XX PD 16-MAY-2002.
XX
XX PF 31-OCT-2000; 2000WO-US41717.
XX
XX PR 31-OCT-2000; 2000WO-US41717.
XX
XX PA (GEO) GEN HOSPITAL CORP.
XX
XX PI Szostak JW, Wilson DS, Keefe AD;
XX
XX DR WPI; 2002-500155/53.
XX

PT Novel peptide with high affinity for streptavidin, is expressed as part
PT of fusion protein to facilitate detection, quantitation and
PT purification of desired protein -
XX
XX Claim 9; Fig 5; 56pp; English.
XX
XX The invention describes a peptide (I) which binds streptavidin with a
CC dissociation constant less than 10 muM or 23 nM, where the amino acid
CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not
CC disulphide bonded or cyclised. A fusion protein comprising a protein of
CC interest covalently linked to (I) is useful for purifying a desired
CC protein from a sample by contacting the sample with streptavidin under
CC conditions that allow complex formation between the fusion protein and
CC the streptavidin, isolating the complex and recovering the fusion
CC protein, and thus purifying the desired protein from the sample. The
CC invention describes a method for producing a streptavidin-binding fusion
CC protein. This sequence represents a truncation mutant of the
CC streptavidin-binding peptide SB-19 isolated from Escherichia coli using a
CC method described in the specification.
XX
XX SQ Sequence 75 AA;
Query Match 80.9%; Score 38; DB 23; Length 75;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDEKTTGWRGHHVVEGLAGELEQLRLARLEHHHPQGOREP 38
DB 1 MDEKTTGWRGHHVVEGLAGELEQLRLARLEHHHPQGOREP 38
RESULT 8
ABU57599
ID ABU57599 standard; Peptide; 75 AA.
XX
XX AC ABU57599;
XX
XX DT 09-APR-2003 (first entry)
XX
XX DE Synthetic peptide SB19 C-terminal deletion mutant, C2.
XX
XX KW Streptavidin-binding peptide; mRNA display; peptide library;
XX fusion protein; mutant; mutein; SB19.
XX
XX OS Synthetic.
XX
XX PN US2002155578-A1.
XX
XX PD 24-OCT-2002.
XX
XX PF 31-OCT-2001; 2001US-0004381.
XX
XX PR 31-OCT-2000; 2000US-244541P.
XX
XX PA (SZOS/) SZOSTAK J W.
XX PA (WILS/) WILSON D S.
XX PA (KEEF/) KEEFE A D.
XX
XX PI Szostak JW, Wilson DS, Keefe AD;
XX
XX DR WPI; 2003-182639/18.
XX
XX PT Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
XX Claim 14; Fig 5; 36pp; English.
XX
XX The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPQ, HPM, HPN or HQP motif. The peptides are generated by the mRNA

display method to create a library of peptides. Also include are a nucleic acid encoding the peptide, a vector comprising the nucleic acid, a fusion protein (and its encoding nucleic acid/vector) comprising a protein of interest covalently linked to the streptavidin binding peptide and detecting the presence of the fusion protein in a sample using streptavidin or streptavidin-containing compounds. The fusion protein (which comprises the desired protein of interest covalently linked to the streptavidin binding peptide) is useful for purifying a protein of interest from a sample, which involves expressing the fusion protein in the sample, contacting the sample with streptavidin under conditions that allow complex formation between the fusion protein and the streptavidin, isolating the complex and recovering the fusion protein, thereby purifying the protein of interest from the sample. The present sequence is a mutated version of S19, a streptavidin binding peptide of the invention. The mutants comprise 3 N-terminal deletions, 3 C-terminal deletions and a truncated N-terminal peptide with point mutations.

SQ Sequence 75 AA;

Query Match	80.9%	Score 38	DB 24	Length 75
Best Local Similarity	100.0%	Pred. No.	7.5e-33	
Matches 38	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLEHHPOGOREP 38
|||||
Db 1 MDEKTTGWRGGHVVEGLAGELEQLRLARLEHHPOGOREP 38

RESULT 9
ABG67076
ID ABG67076 standard; Peptide; 89 AA

DT 24-SEP-2002 (first entry)

Streptavidin-binding peptide SB19 truncation mutant #2

KW Streptavidin-binding peptide; mutant; mutein

OS **Escherichia coli.**

PN W0200238580-A1.

PD 16-MAY-2002

PF 31-OCT-2000; 2000WO-US41717

PR 31-OCT-2000; 2000WO-US41717

PA (GEHO) GEN HOSPITAL CORP

PI Szostak JW, Wilson DS, Keefe AD

DR WPI; 2002-500155/53.

PT Novel peptide with high affinity for streptavidin, is expressed as part
PT of fusion protein to facilitate detection, quantitation and
PT purification of desired protein -

PS Claim 9; Fig 5; 56pp; English.

CC The invention describes a peptide (I) which binds streptavidin with a
CC dissociation constant less than 10 μM or 23 nM, where the amino acid
CC sequence of (I) does not contain an HPO, HPM, HPN or HQP motif, is not
CC disulfide bonded or cyclized. A fusion protein comprising a protein of
CC interest covalently linked to (I) is useful for purifying a desired
CC protein from a sample by contacting the sample with streptavidin under
CC conditions that allow complex formation between the fusion protein and
CC the streptavidin, isolating the complex and recovering the fusion
CC protein, and thus purifying the desired protein from the sample. The
CC invention describes a method for producing a streptavidin-binding fusion

CC protein. This sequence represents a truncation mutant of the
CC streptavidin-binding peptide SB-19 isolated from *Escherichia coli*, using a
CC method described in the specification.

SQ **Sequence** **89 AA;**

Query Match	80.9%	Score 38;	DB 23;	length 89;
Best Local Similarity	100.0%	Pred. No. 8.8e-33;		
Matches 38;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1 MDEKTTGWRGGHVEGLAGELFQLRLARLEHHPOGOREP 38
Db	1 MDEKTTGWRGGHVEGLAGELFQLRLARLEHHPOGOREP 38

RESULT 10
ABU57598

ID ABU57598 standard; Peptide; 89 AA

AC ABU57598;

DT 09-APR-2003 (first entry)

DE Synthetic peptide SB19 C-terminal deletion mutant, C1.

KW Streptavidin-binding peptide; mRNA display; peptide library;

OS Synthetic.

PN US2002155578-A1

PD 24-OCT-2002

PF 31-OCT-2001; 2001US-0004381.

PR 31-OCT-2000; 2000US-244541P.

PA (SZOS/) SZOSTAK J W

PA (KEEF/) KEEFE A D.

PI Szostak JW, Wilson DS, Keefe AD,

DR WPI; 2003-182639/18

PT Novel peptide which binds streptavidin with high affinity. useful as

[illegible]

PS Claim 14; Fig 5; 36pp; English.

The invention relates to a peptide which binds streptavidin with a dissociation constant less than 10 micro M, where the peptide is not disulphide bonded or cyclised, or with a dissociation constant less than 10 micro M, where the amino acid sequence of the peptide does not contain an H₂O, H₂N or HOP motif. The peptides are generated by the mRNA display method to create a library of peptides. Also include are a nucleic acid encoding the peptide, a vector comprising the nucleic acid, a fusion protein (and its encoding nucleic acid/vector) comprising a protein of interest covalently linked to the streptavidin binding peptide and detecting the presence of the fusion protein in a sample, using streptavidin or streptavidin-containing compounds. The fusion protein (which comprises the desired protein of interest covalently linked to the streptavidin binding peptide) is useful for purifying a protein of interest from a sample, which involves expressing the fusion protein in the sample, contacting the sample with streptavidin under conditions that allow complex formation between the fusion protein and the streptavidin, isolating the complex and recovering the fusion protein, thereby purifying the protein of interest from the sample. The present sequence is a mutated version of S919, a streptavidin binding peptide of the invention. The mutants comprise 3 N-terminal deletions, 3 C-terminal deletions and a truncated N-terminal peptide with point

CC *mutations.
XX
SQ Sequence 89 AA;

Query Match 80.9%; Score 38; DB 24; Length 89;
Best Local Similarity 100.0%; Pred. No. 8.8e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDEKTTGMRGSHVEGLAGELBQLRLRLEHHHPQGOREP 38
DB 1 MDEKTTGMRGSHVEGLAGELBQLRLRLEHHHPQGOREP 38

RESULT 11
ABG67073
ID ABG67073 standard; Peptide; 101 AA.
XX
AC ABG67073;

DT 24-SEP-2002 (first entry)

DE Streptavidin-binding peptide SB19.

KW Streptavidin-binding peptide.

OS Escherichia coli.

PN WO200238580-A1.

PD 16-MAY-2002.

PF 31-OCT-2000; 2000WO-US41717.

PR 31-OCT-2000; 2000WO-US41717.

PA (GENO) GEN HOSPITAL CORP.

PI Szostak JW, Wilson DS, Keefe AD;

DR WPI; 2002-500155/53.

PT Novel peptide with high affinity for streptavidin, is expressed as part
of fusion protein to facilitate detection, quantitation and
purification of desired protein -

PS Claim 9; Fig 3; 56pp; English.

CC The invention describes a peptide (I) which binds streptavidin with a
disassociation constant less than 10 mM or 23 nM, where the amino acid
sequence of (I) does not contain an HPQ, HPW, HPN or HQP motif, is not
disulfide bonded or cyclised. A fusion protein comprising a protein of
interest covalently linked to (I) is useful for purifying a desired
protein from a sample by contacting the sample with streptavidin under
conditions that allow complex formation between the fusion protein and
the streptavidin, isolating the complex and recovering the fusion
protein, and thus purifying the desired protein from the sample. The
invention describes a method for producing a streptavidin-binding fusion
protein. This sequence represents a streptavidin-binding peptide isolated
from Escherichia coli using a method described in the specification.

SQ Sequence 101 AA;

Query Match 80.9%; Score 38; DB 23; Length 101;
Best Local Similarity 100.0%; Pred. No. 9.9e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDEKTTGMRGSHVEGLAGELBQLRLRLEHHHPQGOREP 38
DB 1 MDEKTTGMRGSHVEGLAGELBQLRLRLEHHHPQGOREP 38

RESULT 12
ABG67075

ID ABG67075 standard; Peptide; 101 AA.
XX
AC ABG67075;

DT 24-SEP-2002 (first entry)

DE Streptavidin-binding peptide SB19 truncation mutant #1.

KW Streptavidin-binding peptide; mutant; mutein.

OS Escherichia coli.

PN Synthetic.

PD WO200238580-A1.

PF 16-MAY-2002.

PR 31-OCT-2000; 2000WO-US41717.

PA (GENO) GEN HOSPITAL CORP.

PI Szostak JW, Wilson DS, Keefe AD;

DR WPI; 2002-500155/53.

PT Novel peptide with high affinity for streptavidin, is expressed as part
of fusion protein to facilitate detection, quantitation and
purification of desired protein -

PS Claim 9; Fig 5; 56pp; English.

CC The invention describes a peptide (I) which binds streptavidin with a
disassociation constant less than 10 mM or 23 nM, where the amino acid
sequence of (I) does not contain an HPQ, HPW, HPN or HQP motif, is not
disulfide bonded or cyclised. A fusion protein comprising a protein of
interest covalently linked to (I) is useful for purifying a desired
protein from a sample by contacting the sample with streptavidin under
conditions that allow complex formation between the fusion protein and
the streptavidin, isolating the complex and recovering the fusion
protein, and thus purifying the desired protein from the sample. The
invention describes a method for producing a streptavidin-binding fusion
protein. This sequence represents a truncation mutant of the
streptavidin-binding peptide SB-19 isolated from Escherichia coli using a
method described in the specification.

SQ Sequence 101 AA;

Query Match 80.9%; Score 38; DB 23; Length 101;
Best Local Similarity 100.0%; Pred. No. 9.9e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDEKTTGMRGSHVEGLAGELBQLRLRLEHHHPQGOREP 38
DB 1 MDEKTTGMRGSHVEGLAGELBQLRLRLEHHHPQGOREP 38

RESULT 13
ABU57595
ID ABU57595 standard; Peptide; 101 AA.
XX
AC ABU57595;

DT 09-APR-2003 (first entry)

DE Streptavidin-binding synthetic peptide SB19.

KW Streptavidin-binding peptide; mRNA display; peptide library;
fusion protein.

OS Synthetic.

XX

PN US2002155578-A1.
XX
PD 24-OCT-2002.
XX
XX 31-OCT-2001; 2001US-0004381.
PF
XX 31-OCT-2000; 2000US-244541P.
PR
XX (SZOS/) SZOSTAK J W.
PA (WILSON) WILSON D S.
XX (KEEFE/) KEEFE A D.
XX
PI Szostak JW, Wilson DS, Keefe AD;
XX WPI; 2003-182639/18.
DR
XX
XX Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
PS Claim 14; Fig 3; 36pp; English.
XX
XX The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPO, HPW, HPN or HQP motif. The peptides are generated by the mRNA
CC display method to create a library of peptides. Also include are a
CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
CC a fusion protein (and its encoding nucleic acid/vector) comprising a
CC protein of interest covalently linked to the streptavidin binding
CC peptide and detecting the presence of the fusion protein in a sample
CC using streptavidin or streptavidin-containing compounds. The fusion
CC protein (which comprises the desired protein of interest covalently
CC linked to the streptavidin binding peptide) is useful for purifying a
CC protein of interest from a sample, which involves expressing the
CC fusion protein in the sample, contacting the sample with streptavidin
CC under conditions that allow complex formation between the fusion protein
CC and the streptavidin, isolating the complex and recovering the fusion
CC protein, thereby purifying the protein of interest from the sample.
CC The present sequence is a streptavidin binding peptide of the invention.
XX
SQ Sequence 101 AA;
Query Match 80.9%; Score 38; DB 24; Length 101;
Best Local Similarity 100.0%; Pred. No. 9.9e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MDEKTTGMRGHHVEGLAGLEQLRLRHHHPQGGREP 38
DB 1 MDEKTTGMRGHHVEGLAGLEQLRLRHHHPQGGREP 38
RESULT 14
ABUS7597
ID ABUS7597 standard; Peptide; 101 AA.
XX
XX ABUS7597;
AC
XX
XX 09-APR-2003 (first entry)
DT
XX
XX Streptavidin-binding synthetic peptide SB19 full length peptide.
DE Streptavidin-binding synthetic peptide; mRNA display; peptide library;
XX fusion protein.
XX
XX Synthetic.
OS
XX US2002155578-A1.
XX
XX 24-OCT-2002.
PD
XX 31-OCT-2001; 2001US-0004381.
PF

XX
XX 31-OCT-2000; 2000US-244541P.
PR
XX
XX (SZOS/) SZOSTAK J W.
PA (WILSON) WILSON D S.
XX (KEEFE/) KEEFE A D.
XX
XX Szostak JW, Wilson DS, Keefe AD;
PI WPI; 2003-182639/18.
XX
XX
XX Novel peptide which binds streptavidin with high affinity useful as
PT affinity tags for purifying fusion proteins containing proteins of
PT interest -
XX
PS Claim 14; Fig 5; 36pp; English.
XX
XX The invention relates to a peptide which binds streptavidin with a
CC dissociation constant less than 10 micro M, where the peptide is not
CC disulphide bonded or cyclised, or with a dissociation constant less than
CC 10 micro M, where the amino acid sequence of the peptide does not contain
CC an HPO, HPW, HPN or HQP motif. The peptides are generated by the mRNA
CC display method to create a library of peptides. Also include are a
CC nucleic acid encoding the peptide, a vector comprising the nucleic acid,
CC a fusion protein (and its encoding nucleic acid/vector) comprising a
CC protein of interest covalently linked to the streptavidin binding
CC peptide and detecting the presence of the fusion protein in a sample
CC using streptavidin or streptavidin-containing compounds. The fusion
CC protein (which comprises the desired protein of interest covalently
CC linked to the streptavidin binding peptide) is useful for purifying a
CC protein of interest from a sample, which involves expressing the
CC fusion protein in the sample, contacting the sample with streptavidin
CC under conditions that allow complex formation between the fusion protein
CC and the streptavidin, isolating the complex and recovering the fusion
CC protein, thereby purifying the protein of interest from the sample.
CC The present sequence is a streptavidin binding peptide of the invention.
XX
SQ Sequence 101 AA;
Query Match 80.9%; Score 38; DB 24; Length 101;
Best Local Similarity 100.0%; Pred. No. 9.9e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MDEKTTGMRGHHVEGLAGLEQLRLRHHHPQGGREP 38
DB 1 MDEKTTGMRGHHVEGLAGLEQLRLRHHHPQGGREP 38
RESULT 15
ABG67091
ID ABG67091 standard; Protein; 426 AA.
XX
XX ABG67091;
AC
XX
XX 24-SEP-2002 (first entry)
DT
XX
XX Maltose-binding protein/Streptavidin-binding peptide fusion protein #2.
DE Streptavidin-binding peptide; maltose-binding protein;
XX hexahistidine tag.
XX
XX Escherichia coli.
OS
XX WO200238580-A1.
XX
XX 16-MAY-2002.
PD
XX
XX 31-OCT-2000; 2000WO-US41717.
PR
XX 31-OCT-2000; 2000WO-US41717.
XX
XX (GENO) GEN HOSPITAL CORP.
XX

PI .Szostak JW, Wilson DS, Keefe AD;
XX
DR WPI: 2002-500155/53.
DR N-PSDB; ABK95732.
XX
PT Novel peptide with high affinity for streptavidin, is expressed as part
PT of fusion protein to facilitate detection, quantitation and
PT purification of desired protein
XX
PS Disclosure; Fig 9B; 56pp; English.
XX
CC The invention describes a peptide (I) which binds streptavidin with a
CC dissociation constant less than 10 mM or 23 nM, where the amino acid
CC sequence of (I) does not contain an HPQ, HPM, HPN or HQP motif, is not
CC disulfide bonded or cyclised. A fusion protein comprising a protein of
CC interest covalently linked to (I) is useful for purifying a desired
CC protein from a sample by contacting the sample with streptavidin under
CC conditions that allow complex formation between the fusion protein and
CC the streptavidin, isolating the complex and recovering the fusion
CC protein, and thus purifying the desired protein from the sample. The
CC invention describes a method for producing a streptavidin-binding fusion
CC protein. This sequence represents a fusion protein comprising
CC maltose-binding protein, a streptavidin-binding peptide, and a
CC hexahistidine tag.
XX
SQ Sequence 426 AA;

Query Match 80.9%; Score 38; DB 23; Length 426;
Best Local Similarity 100.0%; Pred.No. 3.7e-32;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MDEKTTGMRGSHVVEGLAGLEQLRLRLEHHPPGQREP 38
|||
Db 378 MDEKTTGMRGSHVVEGLAGLEQLRLRLEHHPPGQREP 415

Search completed: February 6, 2004, 17:17:37
Job time : 41 secs